



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/803,344

Source:

1FWO

Date Processed by STIC:

3/26/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT

MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/803344

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4      Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text.**
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped  
  
                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                    Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10    Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                    Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 03/26/2004

PATENT APPLICATION: US/10/803,344

TIME: 07:23:05

Input Set : A:\SYR-HDAC-5005-U.ST25.txt

Output Set: N:\CRF4\03262004\J803344.raw

3 <110> APPLICANT: Syrrx, Inc.  
 5 <120> TITLE OF INVENTION: HISTONE DEACETYLASE INHIBITORS  
 7 <130> FILE REFERENCE: SYR-HDAC-5005-U.  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/803,344  
 10 <141> CURRENT FILING DATE: 2004-03-17  
 12 <150> PRIOR APPLICATION NUMBER: US 60/455,437  
 13 <151> PRIOR FILING DATE: 2003-03-17  
 15 <150> PRIOR APPLICATION NUMBER: US 60/531,203  
 16 <151> PRIOR FILING DATE: 2003-12-19  
 18 <160> NUMBER OF SEQ ID NOS: 8  
 20 <170> SOFTWARE: PatentIn version 3.2  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 513  
 24 <212> TYPE: PRT  
 25 <213> ORGANISM: Custom  
 28 <220> FEATURE:  
 W--> 29 <221> NAME/KEY: Residues 1-482 of HDAC1 and a 6-histidine tag at the N-terminus  
 30 <222> LOCATION: (1)..(513)  
 32 <400> SEQUENCE: 1  
 34 Met Ser Tyr Tyr His His His His His Asp Tyr Asp Ile Pro Thr  
 35 1 5 10 15  
 38 Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met  
 39 20 25 30  
 42 Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp Gly  
 43 35 40 45  
 46 Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His  
 47 50 55 60  
 50 Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr Arg  
 51 65 70 75 80  
 54 Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr  
 55 85 90 95  
 58 Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro  
 59 100 105 110  
 62 Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly  
 63 115 120 125  
 66 Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser  
 67 130 135 140  
 70 Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr  
 71 145 150 155 160  
 74 Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser  
 75 165 170 175  
 78 Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu  
 79 180 185 190

pp 1-3,5  
 Does Not Comply  
 Corrected Diskette Needed

invalid <213> response - see item 10 on Error Summary sheet

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/803,344

DATE: 03/26/2004

TIME: 07:23:06

Input Set : A:\SYR-HDAC-5005-U.ST25.txt

Output Set: N:\CRF4\03262004\J803344.raw

```

82 Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
83      195                      200                      205
86 His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
87      210                      215                      220
90 Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
91 225                      230                      235                      240
94 Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
95      245                      250                      255
98 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
99      260                      265                      270
102 Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
103      275                      280                      285
106 Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
107      290                      295                      300
110 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
111 305                      310                      315                      320
114 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile
115      325                      330                      335
118 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
119      340                      345                      350
122 Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
123      355                      360                      365
126 Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
127      370                      375                      380
130 Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
131 385                      390                      395                      400
134 Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
135      405                      410                      415
138 Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Pro
139      420                      425                      430
142 Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
143      435                      440                      445
146 Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn
147      450                      455                      460
150 Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
151 465                      470                      475                      480
154 Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
155      485                      490                      495
158 Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu
159      500                      505                      510
162 Ala

```

166 &lt;210&gt; SEQ ID NO: 2

167 &lt;211&gt; LENGTH: 1542

168 &lt;212&gt; TYPE: DNA

169 &lt;213&gt; ORGANISM: Custom

172 &lt;220&gt; FEATURE:

W--&gt; 173 &lt;221&gt; NAME/KEY: DNA sequence encoding residues 1-482 of HDAC1 and a 6-histidine

W--&gt; 174 tag at the N-terminus

175 &lt;222&gt; LOCATION: (1)..(1542)

## RAW SEQUENCE LISTING

DATE: 03/26/2004

PATENT APPLICATION: US/10/803,344

TIME: 07:23:06

Input Set : A:\SYR-HDAC-5005-U.ST25.txt

Output Set: N:\CRF4\03262004\J803344.raw

177 &lt;400&gt; SEQUENCE: 2

```

178 atgtcgtact accatcacca tcaccatcac gattacgata tcccaacgac cgaaaacctg      60
180 tatttttcagg gcgccatgga acccggggga tccatggcgc agacgcaggg caccgaggagg      120
182 aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccacca      180
184 atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga      240
186 aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc      300
188 gatgactaca ttaaattctt gcgctccatc cgtccagata acatgtcggg gtacagcaag      360
190 cagatgcaga gattcaacgt tgggtgaggac tgtccagtat tcgatggcct gtttgagttc      420
192 tgtcagttgt ctactggtgg ttctgtggca agtgtgtgta aacttaataa gcagcagacg      480
194 gacatcgctg tgaattgggc tgggggcctg caccatgcaa agaagtcgga ggcattctggc      540
196 ttctgttacg tcaatgatat cgtcttgccc atcctggaac tgctaaagta tcaccagagg      600
198 gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggaagaggc cttctacacc      660
200 acggaccggg tcatgactgt gtcctttcat aagtattgag agtacttccc aggaactggg      720
202 gacctaaggg atatcggggc tggcaaaggg aagtattatg ctgttaacta cccgctccga      780
204 gacgggattg atgacagatc ctatgaggcc attttcaagc cggtcatgtc caaagtaatg      840
206 gagatggttc agcctagtgc ggtggtctta cagtgtggct cagactccct atctggggat      900
208 cggttaggtt gcttcaatct aactatcaaa ggacacgcca agtgtgtgga atttgtcaag      960
210 agctttaacc tgcctatgct gatgctggga ggcggtggtt acaccattcg taacgttgcc      1020
212 cgggtgctgga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca      1080
214 tacaatgact actttgaata ctttggaaca gatttcaagc tccacatcag tccttccaat      1140
216 atgactaacc agaacacgaa tgagtacctg gagaagatca aacagcgact gtttgagaac      1200
218 cttagaatgc tgccgcacgc acctggggtc caaatgcagg cgattcctga ggacgccatc      1260
220 cctgaggaga gtggcgatga ggacgaagac gacctgaca agcgcatctc gatctgctcc      1320
222 tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg      1380
224 ggccgcaaga actcttccaa cttcaaaaaa gccaaagagag tcaaaacaga ggatgaaaaa      1440
226 gagaaagacc cagaggagaa gaaagaagtc accgaagagg agaaaaccaa ggaggagaag      1500
228 ccagaagcca aaggggtcaa ggaggaggtc aagttggcct ga      1542

```

231 &lt;210&gt; SEQ ID NO: 3

232 &lt;211&gt; LENGTH: 498

233 &lt;212&gt; TYPE: PRT

234 &lt;213&gt; ORGANISM: Custom

237 &lt;220&gt; FEATURE:

W--&gt; 238 &lt;221&gt; NAME/KEY: Residues 1-488 of HDAC2 and a 6-histidine tag at the C-terminus

239 &lt;222&gt; LOCATION: (1)..(498)

241 &lt;400&gt; SEQUENCE: 3

```

243 Met Gly Ser Met Ala Tyr Ser Gln Gly Gly Gly Lys Lys Lys Val Cys
244 1          5          10          15
247 Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
248          20          25          30
251 Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Asn
252          35          40          45
255 Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
256          50          55          60
259 Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
260 65          70          75          80
263 Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
264          85          90          95
267 Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
268          100          105          110

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/803,344

DATE: 03/26/2004

TIME: 07:23:06

Input Set : A:\SYR-HDAC-5005-U.ST25.txt

Output Set: N:\CRF4\03262004\J803344.raw

```

271 Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
272      115      120      125
275 Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
276      130      135      140
279 His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
280 145      150      155      160
283 Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
284      165      170      175
287 Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
288      180      185      190
291 Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
292      195      200      205
295 Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
296      210      215      220
299 Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
300 225      230      235      240
303 Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
304      245      250      255
307 Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
308      260      265      270
311 Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
312      275      280      285
315 Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
316      290      295      300
319 Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
320 305      310      315      320
323 Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
324      325      330      335
327 Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
328      340      345      350
331 Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
332      355      360      365
335 Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
336      370      375      380
339 Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
340 385      390      395      400
343 Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
344      405      410      415
347 Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
348      420      425      430
351 Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
352      435      440      445
355 Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
356      450      455      460
359 Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr
360 465      470      475      480
363 Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
364      485      490      495
367 His His

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/803,344

DATE: 03/26/2004

TIME: 07:23:06

Input Set : A:\SYR-HDAC-5005-U.ST25.txt

Output Set: N:\CRF4\03262004\J803344.raw

371 &lt;210&gt; SEQ ID NO: 4

372 &lt;211&gt; LENGTH: 1497

373 &lt;212&gt; TYPE: DNA

374 &lt;213&gt; ORGANISM: Custom

377 &lt;220&gt; FEATURE:

W--&gt; 378 &lt;221&gt; NAME/KEY: DNA sequence encoding residues 1-488 of HDAC2 and a 6-histidine

W--&gt; 379 tag at the C-terminus

380 &lt;222&gt; LOCATION: (1)..(1497)

382 &lt;400&gt; SEQUENCE: 4

```

383 atgggatcca tggcgtacag tcaaggaggc ggcaaaaaaa aagtctgcta ctactacgac      60
385 ggtgatattg gaaattatta ttatggacag ggtcatccca tgaagcctca tagaatccgc      120
387 atgaccataa acttgctgtt aaattatggc ttatacagaa aaatggaaat atataggccc      180
389 cataaagcca ctgccgaaga aatgacaaaa tatcacagtg atgagtatat caaatttcta      240
391 cgggtcaataa gaccagataa catgtctgag tatagtaagc agatgcagag atttaattgt      300
393 ggagaagatt gtccagtgtt tgatggactc tttgagtttt gtcagctctc aactggcggt      360
395 tcagtttgctg gagctgtgaa gttaaaaccg caacagactg atatggctgt taattgggct      420
397 ggaggattac atcatgctaa gaaatcagaa gcatcaggat tctgttacgt taatgatatt      480
399 gtgcttgcca tccttgaatt actaaagtat catcagagag tcttatatat tgatatagat      540
401 attcatcatg gtgatgggtg tgaagaagct ttttatacaa cagatcgtgt aatgacggta      600
403 tcattccata aatatgggga atactttcct ggcacaggag acttgagggg tattggtgct      660
405 ggaaaaggca aatactatgc tgtcaatttt ccaatgagag atggtataga tgatgagtca      720
407 tatgggcaga tatttaagcc tattatctca aaggtgatgg agatgtatca acctagtgtc      780
409 gtggtattac agtgtggtgc agactcatta tctggtgata gactggggtt tttcaatcta      840
411 acagtcaaaag gtcattgctaa atgtgtagaa gttgtaaaaa cttttaactt accattactg      900
413 atgcttgagg gaggtggcta cacaatccgt aatgttgctc gatgttggac atatgagact      960
415 gcagttgccc ttgattgtga gattcccaat gagttgccat ataattgatta ctttgagtat      1020
417 tttggaccag acttcaaact gcatattagt ccttcaaaca tgacaaacca gaacactcca      1080
419 gaatatatgg aaaagataaa acagcgtttg tttgaaaatt tgcgcatgtt acctcatgca      1140
421 cctggtgtcc agatgcaagc tattccagaa gatgctgttc atgaagacag tggagatgaa      1200
423 gatggagaag atccagacaa gagaatttct attcgagcat cagacaagcg gatagcttgt      1260
425 gatgaagaat tctcagattc tgaggatgaa ggagaaggag gtcgaagaaa tgtggctgat      1320
427 cataagaaag gagcaaagaa agctagaatt gaagaagata agaaagaaac agaggacaaa      1380
429 aaaacagacg ttaaggaaga agataaatcc aaggacaaca gtggtgaaaa aacagatacc      1440
431 aaaggaacca aatcagaaca gctcagcaac cccgggcata accatcacca tcactaa      1497

```

434 &lt;210&gt; SEQ ID NO: 5

435 &lt;211&gt; LENGTH: 782

436 &lt;212&gt; TYPE: PRT

437 &lt;213&gt; ORGANISM: Custom

440 &lt;220&gt; FEATURE:

W--&gt; 441 &lt;221&gt; NAME/KEY: Residues 73-845 of HDAC6 and a 6-histidine tag at the C-terminus

442 &lt;222&gt; LOCATION: (1)..(782)

444 &lt;400&gt; SEQUENCE: 5

```

446 Met Pro Gly Met Asp Leu Asn Leu Glu Ala Glu Ala Leu Ala Gly Thr
447 1          5          10          15
450 Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp
451          20          25          30
454 Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln
455          35          40          45
458 Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg

```

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

**VERIFICATION SUMMARY**PATENT APPLICATION: **US/10/803,344**

DATE: 03/26/2004

TIME: 07:23:07

Input Set : **A:\SYR-HDAC-5005-U.ST25.txt**Output Set: **N:\CRF4\03262004\J803344.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:29 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:173 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
L:174 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:2  
L:238 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:378 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:379 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:4  
L:441 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:649 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:650 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:6  
L:742 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7  
L:854 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:855 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:8